1

SEQUENCE LISTING

<110> CHAUDHARY, SARITA
      VAN ROOIJEN, GIJS
      MOLONEY, MAURICE
      SINGH, SURINDER

<120> FLAX SEED SPECIFIC PROMOTERS

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<141> 2004-03-19

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ctcttattat atcacaacaa tcaatcaatc ctactcctcc atactcgaac aaatccgacc 1980

aacttatacc aatattccca aacttgatta atttctcagc aat atg gat cag acg   2035
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cac cag aca tac gcc gga acc acg cag aac ccg agc tat ggc ggc ggg   2083
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Gly Thr Met Tyr Gln Gln Gln Gln Pro Arg Ser Tyr Gln Ala Val Lys
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gcg gcc act gca gcc acc gcg ggt gga tcc ctc atc gtt ctg tcc ggt   2179
Ala Ala Thr Ala Ala Thr Ala Gly Gly Ser Leu Ile Val Leu Ser Gly
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ctc atc ctt acg gcc acc gtc att tca ctc atc ata gcc acc cct ctc   2227
Leu Ile Leu Thr Ala Thr Val Ile Ser Leu Ile Ile Ala Thr Pro Leu
             55                  60                  65

ctt gtc atc ttc agc cct gtt ctt gtc ccg gct ctc atc acc gtc ggg   2275
Leu Val Ile Phe Ser Pro Val Leu Val Pro Ala Leu Ile Thr Val Gly
     70                  75                  80

ctc ttg atc acc ggg ttt ctt gct tcc ggt ggg ttc gga gtc gcc gcc   2323
Leu Leu Ile Thr Gly Phe Leu Ala Ser Gly Gly Phe Gly Val Ala Ala
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gtc acc gtc ttg tcc tgg atc tat agg tatgtataag ctttggactt         2370
Val Thr Val Leu Ser Trp Ile Tyr Arg
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cccaacaact cagaactcga gtcagtgggt tgtgacggtt ctctataaac atttcgaaaa 2670

tctttgttca atgaacgtag aaatgaccat gcttgatgat tgtgggtctt ataagg tac 2729
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tcg aag ctg gcc gga aag gcc agg gag gtg aag gac agg gcg tcg gag   2825
Ser Lys Leu Ala Gly Lys Ala Arg Glu Val Lys Asp Arg Ala Ser Glu
             130                 135                 140

ttc gca cag cag cat gtc aca ggt ggt caa cag acc tct taa           2867
Phe Ala Gln Gln His Val Thr Gly Gly Gln Gln Thr Ser
             145                 150                 155
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caagttggag atgtttgtaa cgatgatgtt ttctaataat cagagatatt aaaagggttg 3047

ctaatttagt attgcgtctg atctcggacc aaactcgcaa gtaaaattgc agaggatgag 3107
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Gln Ala Val Lys Ala Ala Thr Ala Ala Thr Ala Gly Gly Ser Leu Ile
        35                  40                  45

Val Leu Ser Gly Leu Ile Leu Thr Ala Thr Val Ile Ser Leu Ile Ile
    50                  55                  60
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Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Val Leu Val Pro Ala Leu
 65                  70              75                  80

Ile Thr Val Gly Leu Leu Ile Thr Gly Phe Leu Ala Ser Gly Gly Phe
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Gly Val Ala Ala Val Thr Val Leu Ser Trp Ile Tyr Arg
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Glu Phe Ala Gln Gln His Val Thr Gly Gly Gln Gln Thr Ser
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ttaattccca tcaagtcttc cttcagctgc gtagcactgc tagctccaac atggagcgtg 300

gagtctactc gttcatgggg catcgcaaag gtttgccttc atgttctgct accagccagc 360

gcccaccgcc tcttggttgt gtggacaatt gcggtgaagc gcgcaagttg acatcccata 420

gtctcgacac ttcaccatat ggatgtttaa aacgtatatc acgagtgcga tctacatgtc 480

ccatcacacc acatataaag caatagtttg ggagcttttc atatttgaaa cgggcattga 540

cgacttgccc tctcgataat ttaatctttt tttctcttca gctgattgtg tgcatccatt 600
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ggtagatcgt atgctagtac ccaaaaatca gtttgtcgta gcggaatcaa cactagagac 780

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cagatcacga atagctaccc ctttttcggg cgccaaattt ccggcatcct atcttccacc 960

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cctttaaaga accaccacgc cacctccctc tcacaaacac tcataaaaaa accacctctt 1800

gcatttctcc caagttcaaa ttagttcaca gctaagcaag aactcaacaa ca atg gcg 1858
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Asp Arg Thr Thr Gln Pro His Gln Val Gln Val His Thr Gln His His
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tat ccc acc ggc ggg gct ttc ggc cgt tat gaa ggt gga ctc aaa ggc   1954
Tyr Pro Thr Gly Gly Ala Phe Gly Arg Tyr Glu Gly Gly Leu Lys Gly
    20   25   30

ggt cca cat cac cag caa gga tca ggc agc ggc cca tca gct tcc aag   2002
Gly Pro His His Gln Gln Gly Ser Gly Ser Gly Pro Ser Ala Ser Lys
 35   40   45   50

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                55                      60                  65

ttg gcc ggg ata acc ttg gct ggg acg atg atc ggg ctg gcg atc acc    2098
Leu Ala Gly Ile Thr Leu Ala Gly Thr Met Ile Gly Leu Ala Ile Thr
                70                      75                  80

acc ccg att ttt gtc atc tgc agc cct gtt cta gtc ccg gcc gct ctg    2146
Thr Pro Ile Phe Val Ile Cys Ser Pro Val Leu Val Pro Ala Ala Leu
                85                      90                  95

ctc atc ggg ttt gcc gtg agc gcg ttt ctg gcc tcg ggg atg gcc ggg    2194
Leu Ile Gly Phe Ala Val Ser Ala Phe Leu Ala Ser Gly Met Ala Gly
        100                     105                     110

ctg aca ggg ctg acc tcg ctg tcg tgg ttt gcg agg tat ctg cag cag    2242
Leu Thr Gly Leu Thr Ser Leu Ser Trp Phe Ala Arg Tyr Leu Gln Gln
115                     120                     125             130

gct ggg cag gga gtt gga gtg ggg gtg ccg gat agt ttc gag cag gcg    2290
Ala Gly Gln Gly Val Gly Val Gly Val Pro Asp Ser Phe Glu Gln Ala
                135                     140                 145

aag agg cgc atg cag gat gct gct ggg tat atg ggg cag aag acc aag    2338
Lys Arg Arg Met Gln Asp Ala Ala Gly Tyr Met Gly Gln Lys Thr Lys
                150                     155                 160

gaa gtt ggg cag gag atc cag agg aag tct cag gat gtg aaa gca tca    2386
Glu Val Gly Gln Glu Ile Gln Arg Lys Ser Gln Asp Val Lys Ala Ser
                165                     170                 175

gac aaa taa ggtgataata aggggttttg ggttcgtgtg taaactggta           2435
Asp Lys
    180

aaatggaaat tctgggtttt actgtacttt tgcatgtagt ggaatgaatg agttcttgtt 2495

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caagaattcg caacaaattt agctaaacca gttcaatctt accggttaga cgacttccca 2615

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gatggttcca ggctaaatcc acaacgctga acaaattaaa agatgaatgg atcaatcttc 3455

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            20                  25                  30

Lys Gly Gly Pro His His Gln Gln Gly Ser Gly Ser Gly Pro Ser Ala
        35                  40                  45

Ser Lys Val Leu Ala Val Met Thr Ala Leu Pro Ile Gly Gly Thr Leu
    50                  55                  60

Leu Ala Leu Ala Gly Ile Thr Leu Ala Gly Thr Met Ile Gly Leu Ala
65                  70                  75                  80

Ile Thr Thr Pro Ile Phe Val Ile Cys Ser Pro Val Leu Val Pro Ala
                85                  90                  95

Ala Leu Leu Ile Gly Phe Ala Val Ser Ala Phe Leu Ala Ser Gly Met
            100                 105                 110

Ala Gly Leu Thr Gly Leu Thr Ser Leu Ser Trp Phe Ala Arg Tyr Leu
        115                 120                 125

Gln Gln Ala Gly Gln Gly Val Gly Val Gly Val Pro Asp Ser Phe Glu
    130                 135                 140

Gln Ala Lys Arg Arg Met Gln Asp Ala Ala Gly Tyr Met Gly Gln Lys
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caccacacga ctcacaactc gactctcaca ccttaaagaa ccaatcacca ccaaaaa   417

atg gca aag ctg atg agc cta gca gcc gta gca acg cag ttc ctc ttc   465
Met Ala Lys Leu Met Ser Leu Ala Ala Val Ala Thr Gln Phe Leu Phe
 1   5   10   15

ctg atc gtg gtg gac gca tcc gtc cga acc aca gtg att atc gac gag   513
Leu Ile Val Val Asp Ala Ser Val Arg Thr Thr Val Ile Ile Asp Glu
            20   25   30

gag acc aac caa ggc cgc ggt gga ggc aag gtg gca ggg aca gca gca   561
Glu Thr Asn Gln Gly Arg Gly Gly Gly Lys Val Ala Gly Thr Ala Ala
        35   40   45

gtc tgc gag cag cag atc cag cag cga gac ttc ctg agg agc tgc cag   609
Val Cys Glu Gln Gln Ile Gln Gln Arg Asp Phe Leu Arg Ser Cys Gln
    50   55   60

cag ttc atg tgg gag aaa gtc cag agg ggc ggc cac agc cac tat tac   657
Gln Phe Met Trp Glu Lys Val Gln Arg Gly Gly His Ser His Tyr Tyr
 65   70   75   80

aac cag ggc cgt gga gga ggc gaa cag agc cag tac ttc gaa cag ctg   705
Asn Gln Gly Arg Gly Gly Gly Glu Gln Ser Gln Tyr Phe Glu Gln Leu
                85   90   95

ttt gtg acg acc tta agc aat tgc gca ccg cgg tgc acc atg cca ggg   753
Phe Val Thr Thr Leu Ser Asn Cys Ala Pro Arg Cys Thr Met Pro Gly
            100   105   110

gac ttg aag cgt gcc atc ggc caa atg agg cag gaa atc cag cag cag   801
Asp Leu Lys Arg Ala Ile Gly Gln Met Arg Gln Glu Ile Gln Gln Gln
        115   120   125

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gga cag cag cag gga cag cag cag gaa gtt cag agg tgg atc cag caa   849
Gly Gln Gln Gln Gly Gln Gln Gln Glu Val Gln Arg Trp Ile Gln Gln
    130             135             140

gct aaa caa atc gct aag gac ctc ccc gga cag tgc cgc acc cag cct   897
Ala Lys Gln Ile Ala Lys Asp Leu Pro Gly Gln Cys Arg Thr Gln Pro
145             150             155             160

agc caa tgc cag ttc cag ggc cag cag caa tct gca tgg ttt tga   942
Ser Gln Cys Gln Phe Gln Gly Gln Gln Gln Ser Ala Trp Phe
            165             170             175

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taataataat gagatgaatg tgttttaagt tagtgtaaca gctgtaataa agagagagag 1062

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            20              25              30

Glu Thr Asn Gln Gly Arg Gly Gly Gly Lys Val Ala Gly Thr Ala Ala
        35              40              45

Val Cys Glu Gln Gln Ile Gln Gln Arg Asp Phe Leu Arg Ser Cys Gln
    50              55              60
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Pro Arg


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Gln Ala Glu Ala Gly Thr Ile Glu Val Trp Asp Gln Asn Arg Gln Gln
    50   55   60

Phe Gln Cys Ala Gly Val Ala Val Val Arg Arg Thr Ile Glu Pro Lys
65   70   75   80

Gly Leu Leu Leu Pro Phe Tyr Ser Asn Thr Pro Gln Leu Ile Tyr Ile
                85   90   `   95

Val Gln

<210> 10
<211> 85
<212> PRT
<213> Linum usitatissimum

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Gly or stop codon (amino acid may not be present)

<400> 10
Gly Arg Gly Val Thr Gly Ile Met Phe Pro Xaa Cys Pro Glu Thr Phe
1   5   10   15

Glu Glu Ser Gln Gln Gln Gly Gln Gln Gly Gln Gln Gly Ser Ser Gln
            20   25   30

Asp Gln His Gln Lys Ile Arg Arg Phe Arg Glu Gly Asp Val Ile Ala
        35   40   45

Val Pro Ala Gly Val Ala His Trp Ser Tyr Asn Asp Gly Asn Glu Pro
    50   55   60

Val Met Ala Ile Val Val His Asp Thr Ser Ser His Leu Asn Gln Leu
65   70   75   80

Asp Asn Asn Pro Arg
                85

<210> 11
<211> 165
<212> PRT
<213> Linum usitatissimum

<400> 11
Asn Phe Tyr Leu Ala Gly Asn Pro Arg Asp Glu Phe Glu Gln Ser Gln
1   5   10   15

Gln Gly Gly Arg Leu Ser Arg Gly Glu Ser Glu Gly Gly Arg Gly Arg
            20   25   30

Arg Glu Pro Leu Gln Pro Ala Thr Thr Ser Ser Cys Gly Ile Asp Ser
        35   40   45

Lys Leu Ile Ala Glu Ala Phe Asn Val Asp Glu Asn Val Ala Arg Arg
    50   55   60

Leu Gln Ser Glu Asn Asp Asn Arg Gly Gln Ile Val Arg Val Glu Gly
65   70   75   80

Glu Leu Asp Ile Val Arg Pro Pro Thr Ser Ile Gln Glu Glu Ser Gln
            85   90   95

Glu Gln Gly Gly Arg Gly Gly Gly Arg Tyr Tyr Ser Asn Gly Val Glu
            100   105   110

Glu Thr Phe Cys Ser Met Arg Leu Ile Glu Asn Ile Gly Asp Pro Ser
            115   120   125

Arg Ala Asp Ile Phe Thr Pro Glu Ala Gly Arg Val Arg Ser Leu Asn
    130   135   140

Ser His Asn Leu Pro Val Leu Gln Trp Ile Gln Leu Ser Ala Glu Arg
145   150   155   160

Gly Val Leu Tyr Asn
                165

<210> 12
<211> 141
<212> PRT
<213> Linum usitatissimum

<400> 12
Glu Ala Ile Arg Leu Pro His Trp Asn Ile Asn Ala His Ser Ile Val
1   5   10   15

Tyr Ala Ile Arg Gly Gln Ala Arg Val Gln Ile Val Asn Glu Glu Gly
            20   25   30

Asn Ser Val Phe Asp Gly Val Leu Gln Glu Gly Gln Val Val Thr Val
            35   40   45

```
Pro Gln Asn Phe Ala Val Val Lys Arg Ser Gln Ser Glu Arg Phe Glu
    50                  55              60

Trp Val Ala Phe Lys Thr Asn Asp Asn Ala Met Val Asn Ser Leu Ala
65              70              75              80

Gly Arg Thr Ser Ala Val Arg Ala Ile Pro Ala Asp Val Leu Ala Asn
                85              90              95

Ala Trp Arg Val Ser Pro Glu Glu Ala Arg Arg Val Lys Phe Asn Arg
            100             105             110

Gln Glu Thr His Leu Ala Ser Thr Arg Gly Gln Ser Arg Ser Pro Gly
        115             120             125

Arg Leu Asn Val Val Lys Glu Val Ile Asn Leu Leu Met
    130             135             140
```

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<210> 13
<211> 11
<212> PRT
<213> Linum usitatissimum

<400> 13
Gln Gln Gln Gly Gln Gln Gln Gly Gln Gln Gln
  1               5                   10


<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 14
tccactatgt aggtcata                                                  18


<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 15
ctttaaggtg tgagagtc                                                  18
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<210> 16
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 16
aggggtgatc gatta                                                    15


<210> 17
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 17
gatagaaccc acacgagc                                                 18


<210> 18
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 18
tatctagact caagcatacg gacaagggt                                     29


<210> 19
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic XbaI
      site

<400> 19
tctaga                                                              6


<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 20
ggttatcatt gtatgaactg a                                          21


<210> 21
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic NcoI
      site

<400> 21
ccatgg                                                           6


<210> 22
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 22
gcaagcttaa tgtgacggtg aaataataac gg                              32


<210> 23
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      HindIII site

<400> 23
aagctt                                                           6


<210> 24
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 24
taggtacctg gcaggtaaag actctgctc                                  29
```

<210> 25
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic KpnI
      site

<400> 25
ggtacc   6